

SEQUENCE LISTING

<110> UEMURA, Hidetoshi
OKUI, Akira
KOMINAMI, Katsuya
YAMAGUCHI, Nozomi
MITSUI, Shinichi

<120> NOVEL SERINE PROTEASE BSSP6

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<140> 09/856,320

<141> 2001-05-21

<150> JP 10-347802

<151> 1998-11-20

<160> 41

<170> PatentIn version 3.1

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Met Gln

agg ttg agg tgg ctg cgg gac tgg aag tca tcg ggc aga ggt ctc aca 166
Arg Leu Arg Trp Leu Arg Asp Trp Lys Ser Ser Gly Arg Gly Leu Thr
-50 -45 -40

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Ala Ala Lys Glu Pro Gly Ala Arg Ser Ser Pro Leu Gln Ala Met Arg
-35 -30 -25 -20

att ctg cag tta atc ctg ctt gct ctg gca aca ggg ctt gta ggg gga 262
Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val Gly Gly
-15 -10 -5

gag acc agg atc atc aag ggg ttc gag tgc aag cct cac tcc cag ccc 310
Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser Gln Pro
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Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu	Leu	Cys	Gly	Ala	Thr			
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ctc	atc	gcc	ccc	aga	tgg	ctc	ctg	aca	gca	gcc	cac	tgc	ctc	aag	ccc	406		
Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala	Ala	His	Cys	Leu	Lys	Pro	45		
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cgc	tac	ata	gtt	cac	ctg	ggg	cag	cac	aac	ctc	cag	aag	gag	gag	ggc	454		
Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His	Asn	Leu	Gln	Lys	Glu	Glu	Gly	60		
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Cys	Glu	Gln		Arg	Thr	Ala	Thr	Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	75		
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Asn	Asn	Ser	Leu	Pro	Asn	Lys	Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	90		
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Lys	Met	Ala	Ser	Pro	Val	Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	105		
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ctc	tcc	tca	cgc	tgt	gtc	act	gct	ggc	acc	agc	tgc	ctc	att	tcc	ggc	646		
Leu	Ser	Ser	Arg	Cys	Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	125		
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tgg	ggc	agc	acg	tcc	agc	ccc	cag	tta	cgc	ctg	cct	cac	acc	ttg	cga	694		
Trp	Gly	Ser	Thr	Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	140		
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tgc	gcc	aac	atc	acc	atc	att	gag	cac	cag	aag	tgt	gag	aac	gcc	tac	742		
Cys	Ala	Asn	Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	155		
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Pro	Gly	Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	170		
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ggc	aag	gac	tcc	tgc	cag	ggt	gac	tcc	ggg	ggc	cct	ctg	gtc	tgt	aac	838		
Gly	Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	185		
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cag	tct	ctt	caa	ggc	att	atc	tcc	tgg	ggc	cag	gat	ccg	tgt	gcg	atc	886		
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	Ile	205		
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acc	cga	aag	cct	ggt	gtc	tac	acg	aaa	gtc	tgc	aaa	tat	gtg	gac	tgg	934		
Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	Asp	Trp	220		
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atc	cag	gag	acg	atg	aag	aac	aat	tagactggac	ccaccaccca	cagcccatca						988		
Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn										225	
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 -35 -30 -25

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val
 -20 -15 -10

Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser
 -5 -1 1 5 10

Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly
 15 20 25

Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu
 30 35 40

Lys Pro Arg Tyr Ile Val His Leu Gly Gln His Asn Leu Gln Lys Glu
 45 50 55

Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro
 60 65 70 75

Gly Phe Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met
 80 85 90

Leu Val Lys Met Ala Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro
 95 100 105

Leu Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile
 110 115 120

Ser Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr
 125 130 135

Leu Arg Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn
 140 145 150 155

Ala Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln
160 165 170

Glu Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
175 180 185

Cys Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys
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Asp Trp Ile Gln Glu Thr Met Lys Asn Asn
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Met Arg Arg Leu
-45

aag agt gac tgg aaa tta tct aca gaa acc agg gaa cct ggc gcc cgc 162
Lys Ser Asp Trp Lys Leu Ser Thr Glu Thr Arg Glu Pro Gly Ala Arg
-40 -35 -30

cct gcc cta ctc cag gcc agg atg att ctc cga ctc att gca ctt gct 210
Pro Ala Leu Leu Gln Ala Arg Met Ile Leu Arg Leu Ile Ala Leu Ala
-25 -20 -15

ctg gta aca ggg cac gta ggg gga gag acg agg atc atc aag ggt tat 258
Leu Val Thr Gly His Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Tyr
-10 -5 -1 1 5

gag tgc agg cct cac tca cag cca tgg cag gtg gcc ctc ttt cag aag 306
Glu Cys Arg Pro His Ser Gln Pro Trp Gln Val Ala Leu Phe Gln Lys
10 15 20

aca cgg ctt ctc tgt ggg gca acc ctc atc gcc ccc aaa tgg ctc ctg 354
Thr Arg Leu Leu Cys Gly Ala Thr Leu Ile Ala Pro Lys Trp Leu Leu

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aca gca gcc cac tgc cgc aag ccc cat tac gtg atc ctc ctt gga gag			402
Thr Ala Ala His Cys Arg Lys Pro His Tyr Val Ile Leu Leu Gly Glu			
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cac aat cta gag aag aca gac ggc tgt gag cag agg cgg atg gcc act			450
His Asn Leu Glu Lys Thr Asp Gly Cys Glu Gln Arg Arg Met Ala Thr			
55	60	65	
gag tcc ttc ccc cac ccc gac ttc aac aac agc ctc ccc aac aaa gac			498
Glu Ser Phe Pro His Pro Asp Phe Asn Asn Ser Leu Pro Asn Lys Asp			
70	75	80	85
cac cgg aat gac ata atg ctt gtg aag atg tcg tct ccc gtc ttc ttt			546
His Arg Asn Asp Ile Met Leu Val Lys Met Ser Ser Pro Val Phe Phe			
90	95	100	
acc cga gct gtg cag cca ctc acc ctg tcc cca cac tgt gtc gct gca			594
Thr Arg Ala Val Gln Pro Leu Thr Leu Ser Pro His Cys Val Ala Ala			
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Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Thr Thr Ser Ser Pro Gln			
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Leu Arg Leu Pro His Ser Leu Arg Cys Ala Asn Val Ser Ile Ile Glu			
135	140	145	
cac aag gag tgt gag aag gcc tac ccg ggc aac atc aca gac acc atg			738
His Lys Glu Cys Glu Lys Ala Tyr Pro Gly Asn Ile Thr Asp Thr Met			
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ctg tgc gcc agt gtt cgg aaa gag ggc aag gac tcc tgt cag ggt gac			786
Leu Cys Ala Ser Val Arg Lys Glu Gly Lys Asp Ser Cys Gln Gly Asp			
170	175	180	
tct gga ggc ccc ctg gtc tgc aac gga tct ctt caa ggc atc atc tcc			834
Ser Gly Gly Pro Leu Val Cys Asn Gly Ser Leu Gln Gly Ile Ile Ser			
185	190	195	
tgg ggt cag gac cca tgt gcc gtc acc aga aag cct ggt gtc tat aca			882
Trp Gly Gln Asp Pro Cys Ala Val Thr Arg Lys Pro Gly Val Tyr Thr			
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aaa gtc tgc aaa tac ttt aac tgg atc cac gag gtt atg agg aac aat			930
Lys Val Cys Lys Tyr Phe Asn Trp Ile His Glu Val Met Arg Asn Asn			
215	220	225	
tagaggggac ctgcttccca ccaccaacc cctccaacct cttcttaatg ctttgacttc			990
tcttcattct gccctaagaa gtcctcagct gggaccctgg catgtactct ctccgaccca			1050
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cctgacttga actaaattgt gactctggac atgatcacca ctggttttgt ttgtttggtt			1170
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 -15 -10 -5 -1 1

Ile Lys Gly Tyr Glu Cys Arg Pro His Ser Gln Pro Trp Gln Val Ala
 5 10 15

Leu Phe Gln Lys Thr Arg Leu Leu Cys Gly Ala Thr Leu Ile Ala Pro
 20 25 30

Lys Trp Leu Leu Thr Ala Ala His Cys Arg Lys Pro His Tyr Val Ile
 35 40 45

Leu Leu Gly Glu His Asn Leu Glu Lys Thr Asp Gly Cys Glu Gln Arg
 50 55 60 65

Arg Met Ala Thr Glu Ser Phe Pro His Pro Asp Phe Asn Asn Ser Leu
 70 75 80

Pro Asn Lys Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ser Ser
 85 90 95

Pro Val Phe Phe Thr Arg Ala Val Gln Pro Leu Thr Leu Ser Pro His
 100 105 110

Cys Val Ala Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Thr Thr
 115 120 125

Ser Ser Pro Gln Leu Arg Leu Pro His Ser Leu Arg Cys Ala Asn Val
 130 135 140 145

Ser Ile Ile Glu His Lys Glu Cys Glu Lys Ala Tyr Pro Gly Asn Ile
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Thr Asp Thr Met Leu Cys Ala Ser Val Arg Lys Glu Gly Lys Asp Ser
 165 170 175

Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gly Ser Leu Gln
180 185 190

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Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val Gly Gly
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Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser Gln Pro
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Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala Thr
15 20 25

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Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys Pro
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Trp Val Ser Leu Thr Ser Pro Thr His Val Ser Pro Asp Leu Ser Ser
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tcc aac tac tgt ctc tcc cac ctc agc cgc tac ata gtt cac ctg ggg 344
Ser Asn Tyr Cys Leu Ser His Leu Ser Arg Tyr Ile Val His Leu Gly
65 70 75

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gag cac cag aag tgt gag aac gcc tac ccc ggc aac atc aca gac acc Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly Asn Ile Thr Asp Thr 175 180 185	680
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gac tcc ggg ggc cct ctg gtc tgt aac cag tct ctt caa ggc att atc Asp Ser Gly Gly Pro Leu Val Cys Asn Gln Ser Leu Gln Gly Ile Ile 210 215 220	776
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Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly
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Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu
 30 35 40

Lys Pro Trp Val Ser Leu Thr Ser Pro Thr His Val Ser Pro Asp Leu
 45 50 55

Ser Ser Ser Asn Tyr Cys Leu Ser His Leu Ser Arg Tyr Ile Val His
 60 65 70 75

Leu Gly Gln His Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg
 80 85 90

Thr Ala Thr Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro
 95 100 105

Asn Lys Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro
 110 115 120

Val Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys
 125 130 135

Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr Ser
 140 145 150 155

Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn Ile Thr
 160 165 170

Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly Asn Ile Thr
 175 180 185

Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly Gly Lys Asp Ser Cys
 190 195 200

Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gln Ser Leu Gln Gly
 205 210 215

Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala Ile Thr Arg Lys Pro Gly
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Val Tyr Thr Lys Val Cys Lys Tyr Val Asp Trp Ile Gln Glu Thr Met
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Lys Asn Asn

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<220>
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<210> 9
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<400> 9
ttggtgcatg gcgga                                                            15

<210> 10
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify neurosin-encoding sequence

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tcctcgagac ttggcctgaa tggtttt                                             27

<210> 11
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<212> DNA
<213> Artificial Sequence

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<220>
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 SecTrypHis/Neurosin

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 tgaagcttgc catggaccaa cttgtcatc 29

 <210> 13
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 ccaagcttca ccatcaccat caccat 26

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 <400> 16
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 <210> 17
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 <220>
 <223> Designed oligonucleotide primer to amplify active hBSSP6-encoding sequence

 <400> 17
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 <400> 18
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 <210> 19
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 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 19
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 <210> 20
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as hBSSP6F3 to amplify full-length human brain BSSP6-encoding mRNA (forward)

 <400> 20
 ggactcaaga gaggaacctg 20

<210> 21
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as hBSSP6F4 to amplify
 mature human BSSP6-encoding region (forward)

 <400> 21
 atcatcaagg ggttcgagtg 20

 <210> 22
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as hBSSP6F5 to amplify
 full-length human prostate BSSP6-encoding mRNA (forward)

 <400> 22
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 <210> 23
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as hBSSP6R1 for RACE f
 or human BSSP6 (reverse)

 <400> 23
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 <210> 24
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as hBSSP6R2 for RACE f
 or human BSSP6 (reverse)

 <400> 24
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 <210> 25
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as hBSSP6R3/P to ampli
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 <400> 25
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<210> 26
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<220>
<223> Designed oligonucleotide primer designated as mBSSP6F1 for RACE f
      or mouse BSSP6 (forward)

<400> 26
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<210> 27
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<223> Designated oligonucleotide primer designated as mBSSP6F2 for RACE
      for mouse BSSP6 (forward)

<400> 27
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<210> 28
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<220>
<223> Designed oligonucleotide primer designated as mBSSP6F3 to amplify
      full-length mouse prostate BSSP6-encoding mRNA (forward)

<400> 28
taagctagga gaactgaggc                                     20

<210> 29
<211> 18
<212> DNA
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<220>
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<210> 30
<211> 19
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<220>
<223> Designed oligonucleotide primer designated as mBSSP6F5 to amplify
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<210> 31
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<212> DNA
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<220>
<223> Designed oligonucleotide primer designated as mBSSP6R1 for RACE f
or mouse BSSP6 (reverse)

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<210> 32
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<212> DNA
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<220>
<223> Designed oligonucleotide primer designated as mBSSP6R2 for RACE f
or mouse BSSP6 (reverse)

<400> 32
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<210> 33
<211> 28
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<220>
<223> Designed oligonucleotide primer designated as mBSSP6R3/E to ampli
fy full-length mouse BSSP6-encoding mRNA (reverse)

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<210> 34
<211> 20
<212> DNA
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<220>
<223> Designed oligonucleotide primer designated as hBSSP6R3 to amplify
a portion of BSSP6 variant type-encoding mRNA from human prostat
ic cancer cell line PC-3 (reverse)

<400> 34
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<210> 35
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<220>

<223> Designed oligonucleotide primer designated as hBSSP6F7 to amplify a portion of human BSSP6-encoding mRNA (forward)

<400> 35
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<210> 36
<211> 20
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<223> Designed oligonucleotide primer to amplify conserved region of serin proteases-encoding sequence

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<220>
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<400> 36
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<210> 37
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<212> DNA
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<400> 37
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<210> 38
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<220>

<223> Designed oligonucleotide to construct plasmid pTrypHis
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<210> 39
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide to construct plasmid pTrypHis
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<220>
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<400> 40

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<210> 41
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<220>
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<400> 41

Lys Val His Gly
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